Amendments to the Specification:

Please amend the paragraph that begins on page 12, line 22 as follows:

FIGS 3A-3C: The structure and homologies of the dsc-4 gene and protein product. **(A)** A portion of the primary structure of DSC-4 polypeptide (SEQ ID NO:~~2~~3) aligned with the zebrafish (SEQ ID No:4), mouse (SEQ ID NO:5) and human MTP (SEQ ID NO:6). Identical residues are cross-hatched and residues that have >75% and >50% similarity are in black and in light grey, respectively. The asterisks indicate the mutation sites at which mutations were found in dsc-4 (qm182). There was a C → T transition at position 354 of the gene results in a serine to phenylalanine substitution at position 62 of the protein and a G → A transition at position 605 of the gene results in an alanine to threonine substitution at position 146 of the protein. The signal sequence is not shown. Domains of DSC-4 include: the apoB binding domain (amino acid residues 19-295), the apoB and PDI binding domain (amino acid residues 296-609), and the lipid binding domain (amino acid residues 610-890). **(B)** The genomic structure of dsc-4 gene. The filled-in and open boxes correspond to non-coding and coding regions, respectively. Sequencing of a cDNA as well as a PCR product amplified from a first-strand cDNA library revealed that the dsc-4 message is SL1 trans-spliced and contains 11 exons. **(C)** Schematic representation of the dsc-4 protein. Cross-hatched boxes represent the signal sequence, apoB binding domain, apoB and PDI binding domain and lipid binding and transfer domain.

Please amend the paragraph that begins on page 16, line 19 as follows:

FIG. 10: The amino acid sequence of DSC-3 (SEQ ID NO:8). The amino acid sequence comprises the predicted amino acid sequence of H06H21.10 from the internet database, wormbase ~~(www.wormbase.org)~~ and 92 additional amino acids (amino acids 154-245) . These 92 amino acids were identified by a tBlastn search of the worm genomic sequence using the sequence of the human ATP8B4 protein as a query.

Please amend the paragraph that begins on page 16, line 25 as follows:

FIG. 11: Alignment of the amino acid sequences of the gene dsc-3, four homologous Type IV P-Type ATPases from humans, and consensus sequence. FIC1/PFIC1/BRIC corresponds to ATP8B1 (SEQ ID NO:9), which shares highest amino acid identity with ATP8B2 (SEQ ID NO:10) and ATP8B4 (SEQ ID NO:12). The percent identity of dsc-3 (amino acid positions 35-1127) and AT8B1 (amino acid positions 91-1163) is 50%. The

percent identity of dsc-3 (amino acid positions 20-1172) and ATP8B2 (amino acid positions 46-1161) is 56%. The percent identity of dsc-3 (amino acid positions 25-812) and ATP8B3 (SEQ ID NO:11; amino acid positions 194-1034) is 38%. The percent identity of dsc-3 (amino acid positions 137-1115) and ATP8B4 (2 to 946) is 54%.

Please amend the paragraph that begins on page 68, line 15 as follows:

Examples of somatic indicator genes including, but not limited to, myo-3 (body wall muscle), elt-2 (gut), myo-2 (pharynx), dpy-7 (hypodermis). Examples of tissue and cell specific indicator genes have been described in publicly accessible databases (*e.g.* Wormbase~~,~~ ~~http://www.wormbase.org/~~; NEXTDB~~, http://nematode.lab.nig.ac.jp/~~; The Hope Laboratory Expression Pattern Database~~, http://129.11.204.86:591/default.htm~~).

Please amend the paragraph that begins on page 72, line 32 as follows:

In another embodiment, the method comprises detecting the expression of a reporter encoded by a reporter gene that is operably linked to the regulatory sequences of an indicator gene of which the expression level is associated with defecation. Additionally, an expression profile of indicator genes may be used. Exemplary indicator genes of which the promoter can be used include those described in publicly accessible databases (*e.g.* Wormbase, ~~http://www.wormbase.org/~~; NEXTDB~~, http://nematode.lab.nig.ac.jp/~~; The Hope Laboratory Expression Pattern Database~~, http://129.11.204.86:591/default.htm~~).

Please amend the paragraph that begins on page 74, line 15 as follows:

In yet another embodiment, the method comprises detecting the expression of a reporter encoded by a reporter gene that is operably linked to the regulatory sequences of an indicator gene of which the expression level is associated with germline development. Additionally, an expression profile of indicator genes may be used. Exemplary indicator genes of which the promoter can be used include, but are not limited to, ark-1, itr-1, and let 60. The experiments described in Section 5.4.2 demonstrate use of such indicator genes the expression level of which is associated with germline development. Other examples of exemplary indicator genes of which the promoter can be used include those disclosed in Reinke *et al.*, 2000, *Mol. Cell* 6:605-16; Colaiacovo *et al.*, *Genetics* 2002 Sep;162:113-28 or in publicly available databases (*e.g.* Wormbase~~, http://www.wormbase.org/~~; NEXTDB, ~~http://nematode.lab.nig.ac.jp/~~; The Hope Laboratory Expression Pattern Database, ~~http://129.11.204.86:591/default.htm~~).

Please amend the paragraph that begins on page 75, line 5 as follows:

In another embodiment, the method comprises detecting the expression of a reporter encoded by a reporter gene that is operably linked to the regulatory sequences of an indicator gene of which the expression level is associated with embryonic development. Additionally, an expression profile of indicator genes may be used. Exemplary indicator genes of which the promoter can be used include those described in publicly accessible databases (*e.g.* Wormbase~~, http://www.wormbase.org/~~; NEXTDB~~, http://nematode.lab.nig.ac.jp/~~; The Hope Laboratory Expression Pattern Database~~, http://129.11.204.86:591/default.htm~~).

Please amend the paragraph that begins on page 75, line 22 as follows:

In another embodiment, the method comprises detecting the expression of a reporter encoded by a reporter gene that is operably linked to the regulatory sequences of an indicator gene of which the expression level is associated with post-embryonic development. Additionally, an expression profile of indicator genes may be used. Exemplary indicator genes of which the promoter can be used include those described in publicly accessible databases (*e.g.* Wormbase~~, http://www.wormbase.org/~~; NEXTDB, ~~http://nematode.lab.nig.ac.jp/~~; The Hope Laboratory Expression Pattern Database~~, http://129.11.204.86:591/default.htm~~).